```
   1 tcttcctacccatctgctccccagagggctgcctgctgtgcacttgggtcctggagcccttctccacccggatagattcctcacccttggcccgcctttg

 101 ccccaccctactctgcccagaagtgcaagagcctaagccgcctccatggccccaggaaggattcaggggagaggccccaaacagggagccacgccagcca

                     -20                     -10
                     MetGluLeuThrGluLeuLeuLeuValValMetLeuLeuLeuThrAlaArgLeuThrLeuSerSerProAlaProProAlaCysAsp
 201 gacaccccggccagaATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCCTCCTGCTTGTG

       10                  20                          30                      40
     LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu
 301 ACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCT

                   50                      60                      70
     ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal
 401 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTG

                80                      90                      100
     MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
 501 ATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCC

       110                     120                     130                     140
     GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe
 601 TTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTT

                   150                     160                     170
     LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu
 701 CCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGCGGGCCCCACCCACCACAGCTGTCCCCAGCAGAACCTCTCTAGTCCTCACACTGAACGAGCTC

                180                     190                     200
     ProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle
 801 CCAAACAGGACTTCTGGATTGTTGGAGACAAACTTCACTGCCTCAGCCAGAACTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGGATTCAGAGCCAAGA

       210                     220                     230                     240
     ProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeuAsnGlyThrArgGlyLeuPhePro
 901 TTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTGGACCAAATCCCCGGATACCTGAACAGGATACACGAACTCTTGAATGGAACTCGTGGACTCTTTCC

                   250                     260                     270
     GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer
1001 TGGACCCTCACGCAGGACCCTAGGAGCCCCGGACATTTCCTCAGGAACATCAGACACAGGCTCCCTGCCACCCAACCTCCAGCCTGGATATTCTCCTTCC

                280                     290                     300
     ProThrHisProProThrGlyGlnTyrThrLeuPheProLeuProProThrLeuProThrProValValGlnLeuHisProLeuLeuProAspProSerAla
1101 CCAACCCATCCTCCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCACCTTGCCCACCCCTGTGGTCCAGCTCCACCCCCTGCTTCCTGACCCTTCTG

       310                     320                     330
     ProThrProThrProThrSerProLeuLeuAsnThrSerTyrThrHisSerGlnAsnLeuSerGlnGluGly
1201 CTCCAACGCCCACCCCTACCAGCCCTCTTCTAAACACATCCTACACCCACTCCCAGAATCTGTCTCAGGAAGGGTAAggttctcagacactgccgacatc

1301 agcattgtctcatgtacagctcccttccctgcagggcgcccctgggagacaactggacaagatttcctactttctcctgaaacccaaagccctggtaaaa

1401 gggatacacaggactgaaaagggaatcatttttcactgtacattataaaccttcagaagctatttttttaagctatcagcaatactcatcagagcagcta

1501 gctctttggtctattttctgcagaaatttgcaactcactgattctctacatgctctttttctgtgataactctgcaaaggcctgggctggcctggcagtt

1601 gaacagagggagagactaaccttgagtcagaaaacagagaaagggtaatttcctttgcttcaaattcaaggcct[illegible]ccaacgcccccatcccctttactat

1701 cattctcagtgggactctgatcccatattcttaacagatctttactcttgagaaatgaataagctttctctcagaaaaaaaaaaaaaaaaaaa
```

FIG. 1

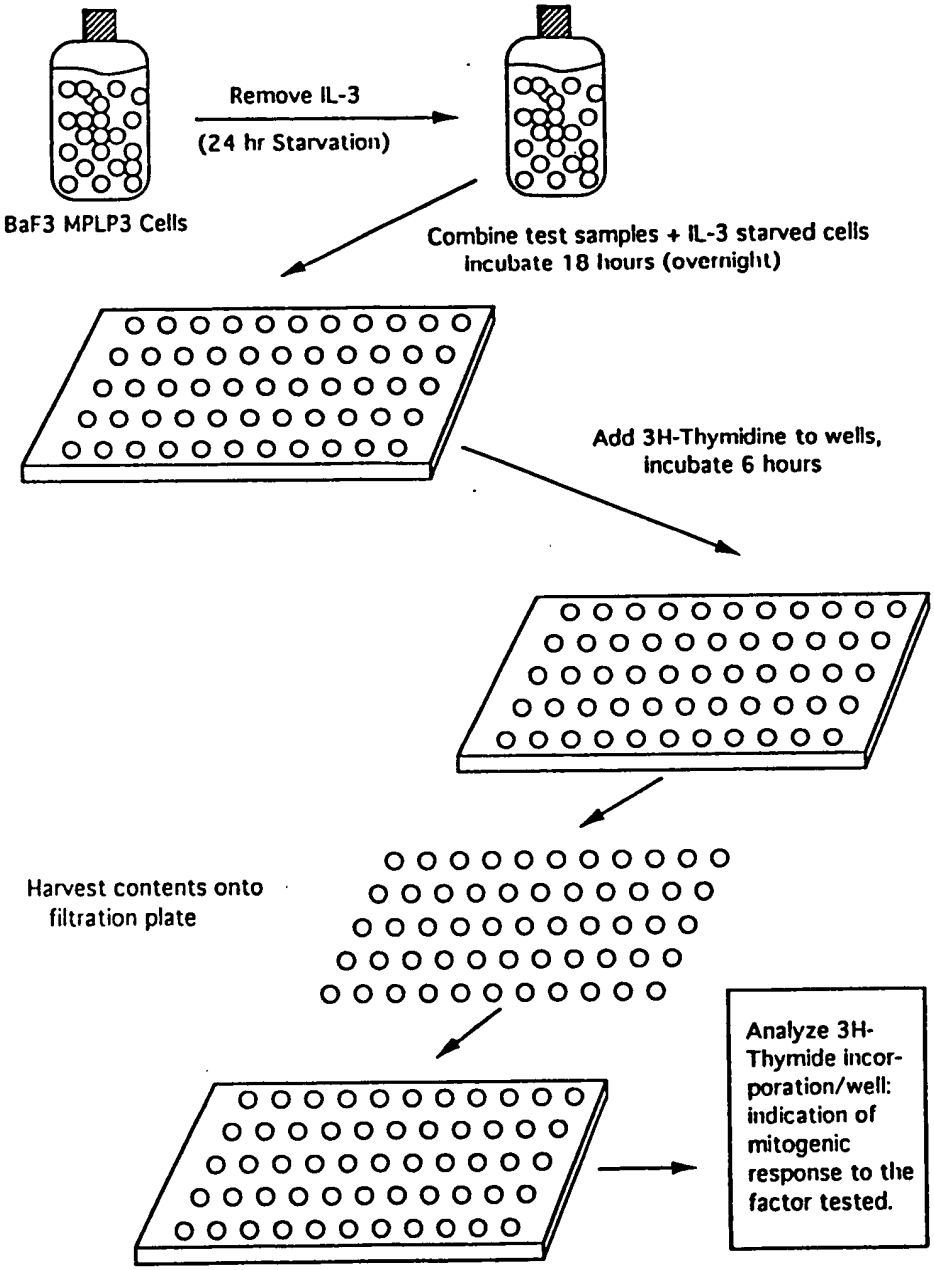

Remove IL-3
(24 hr Starvation)
BaF3 MPLP3 Cells
Combine test samples + IL-3 starved cells
incubate 18 hours (overnight)
Add 3H-Thymidine to wells,
incubate 6 hours
Harvest contents onto
filtration plate
Analyze 3H-
Thymide incor-
poration/well:
indication of
mitogenic
response to the
factor tested.

FIG. 2

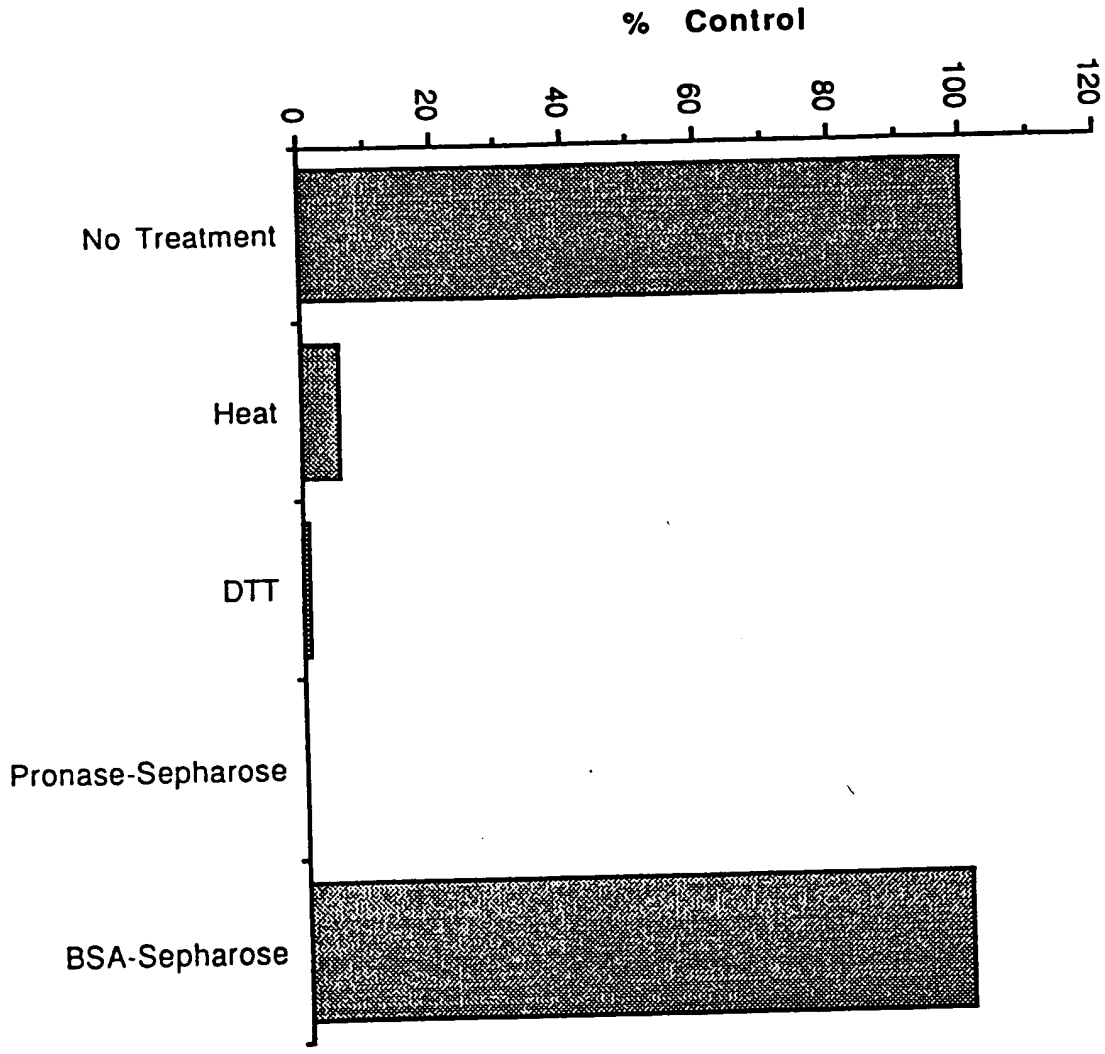

% Control
0
20
40
60
80
100
120
No Treatment
Heat
DTT
Pronase-Sepharose
BSA-Sepharose

FIG. 3

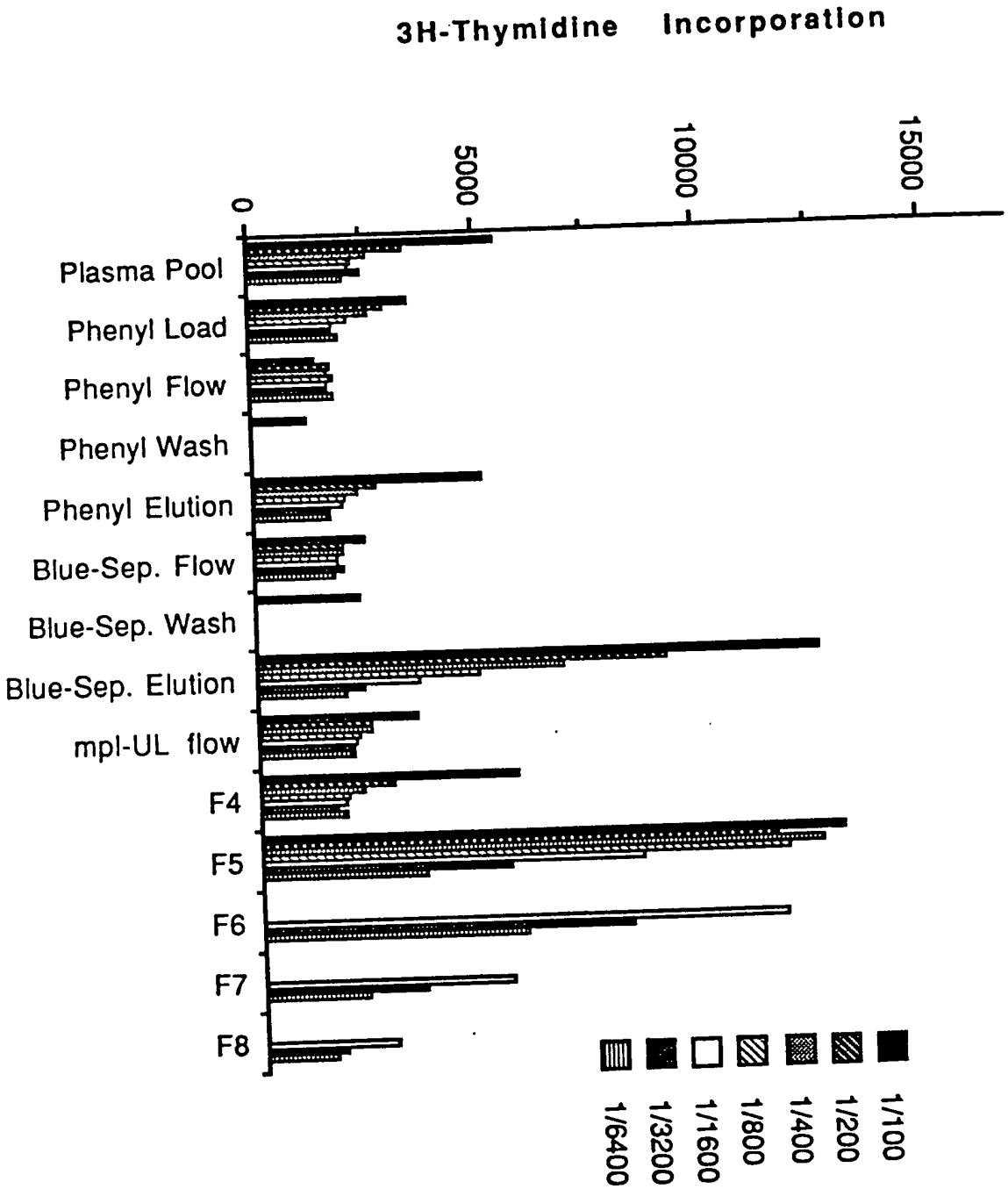

3H-Thymidine Incorporation
0
5000
10000
15000
Plasma Pool
Phenyl Load
Phenyl Flow
Phenyl Wash
Phenyl Elution
Blue-Sep. Flow
Blue-Sep. Wash
Blue-Sep. Elution
mpl-UL flow
F4
F5
F6
F7
F8
1/6400
1/3200
1/1600
1/800
1/400
1/200
1/100

FIG. 4

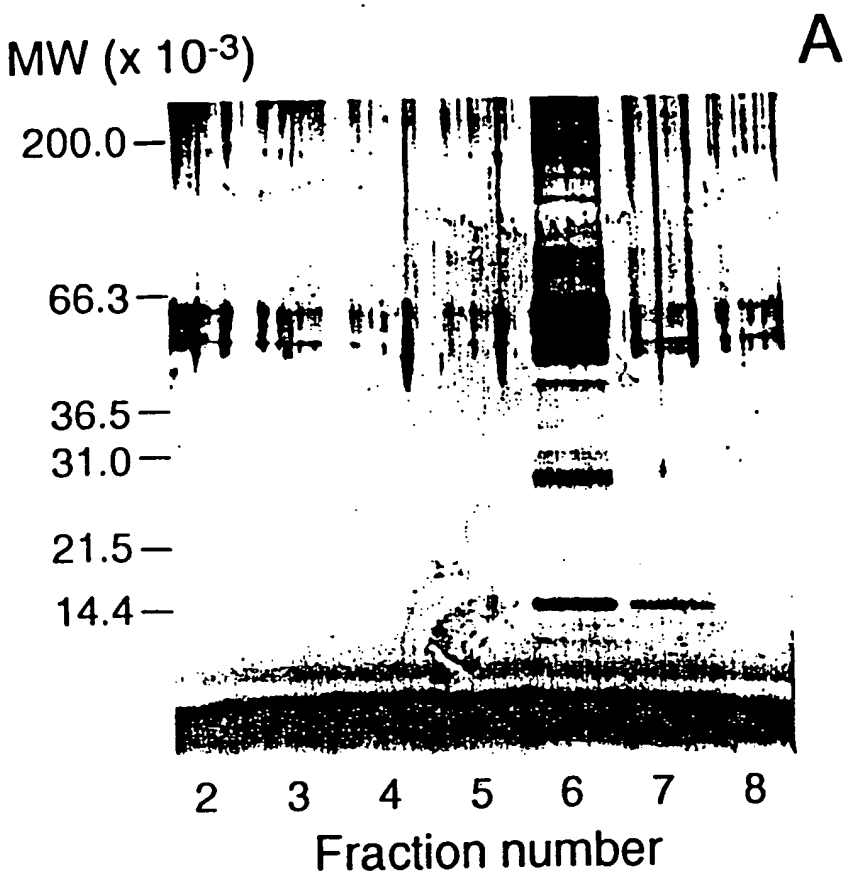


FIG. 5

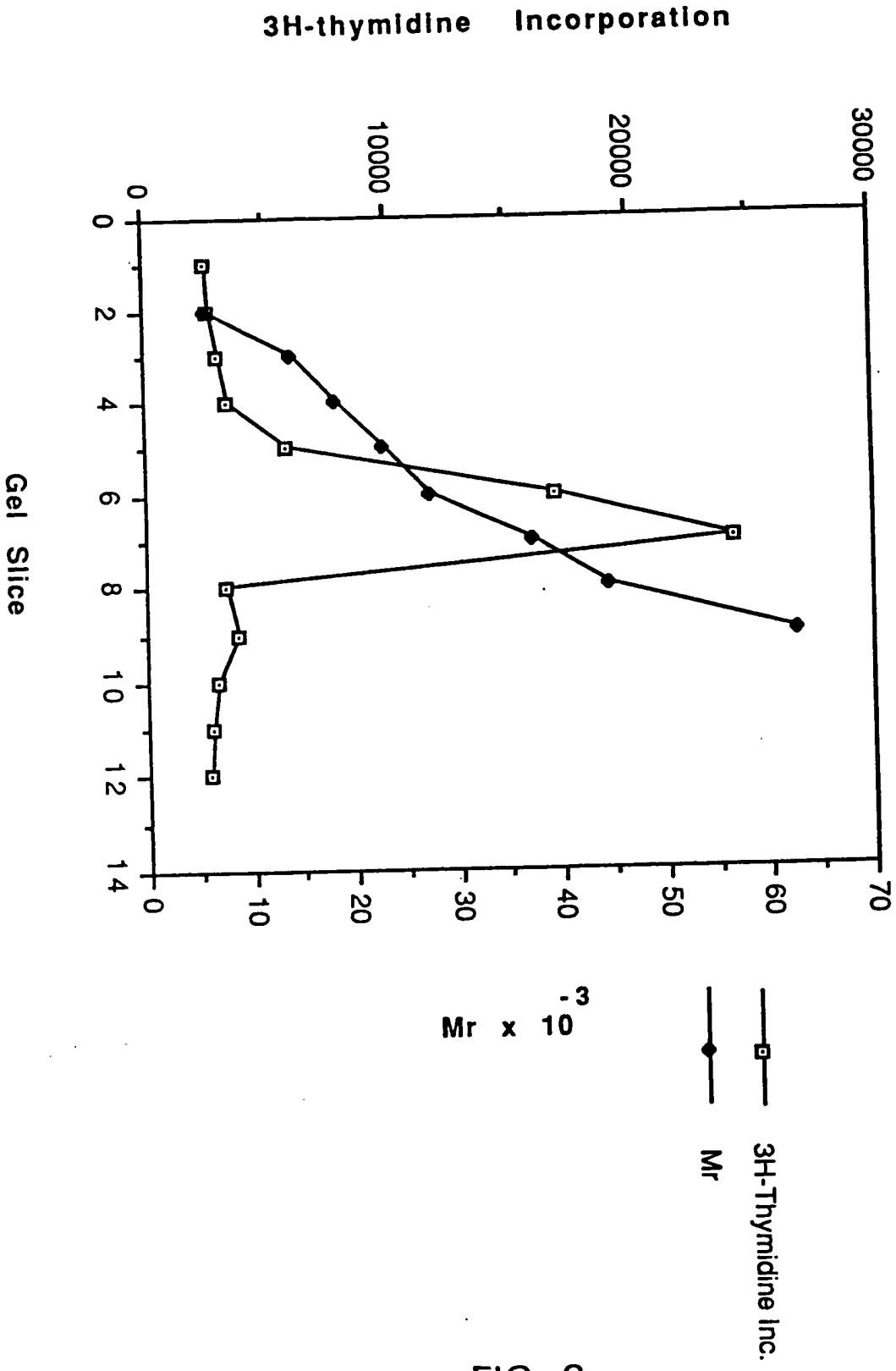

3H-thymidine Incorporation
Gel Slice
Mr x 10 -3
3H-Thymidine Inc.
Mr

FIG. 6

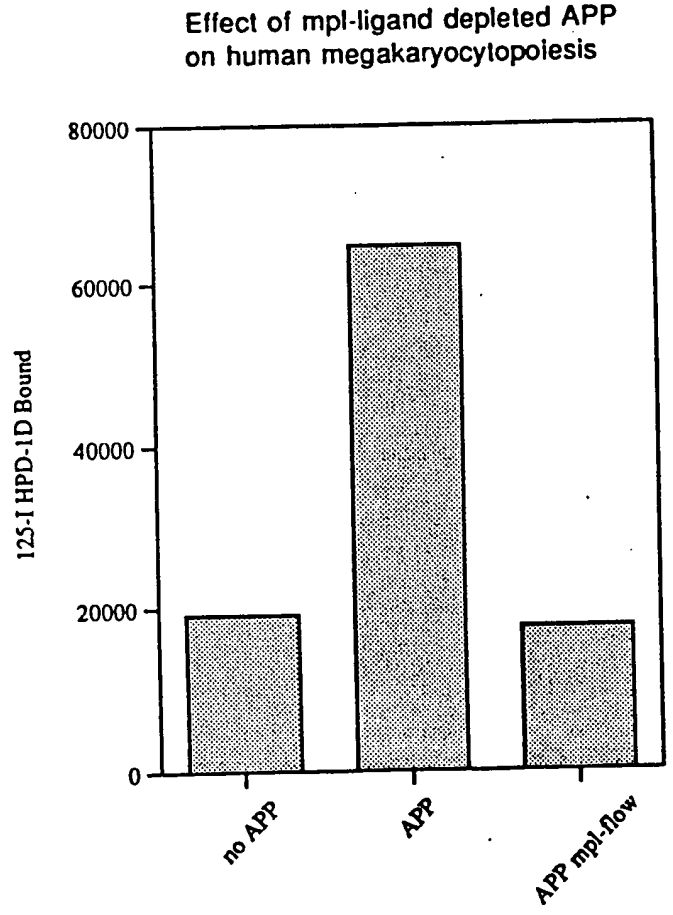

Effect of mpl-ligand depleted APP
on human megakaryocytopoiesis
125-I HPD-1D Bound
80000
60000
40000
20000
0
no APP
APP
APP mpl-flow

FIG. 7

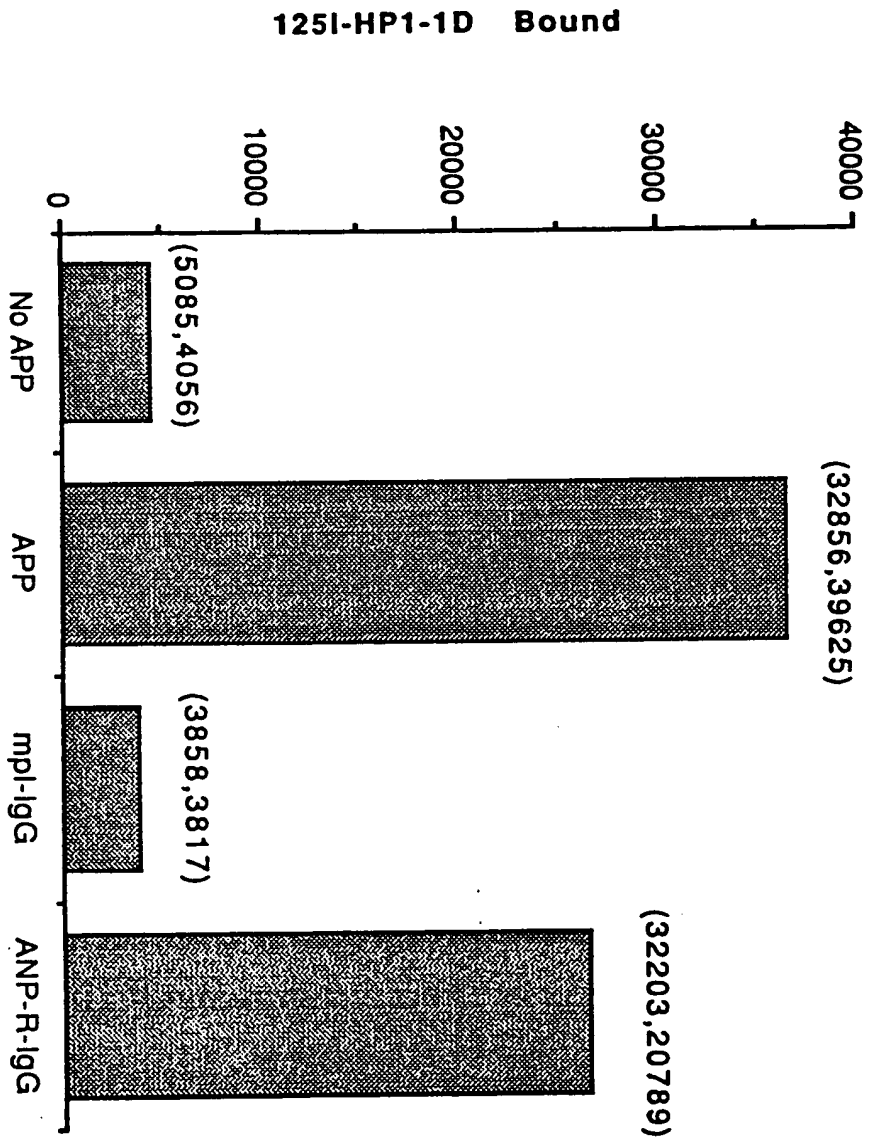
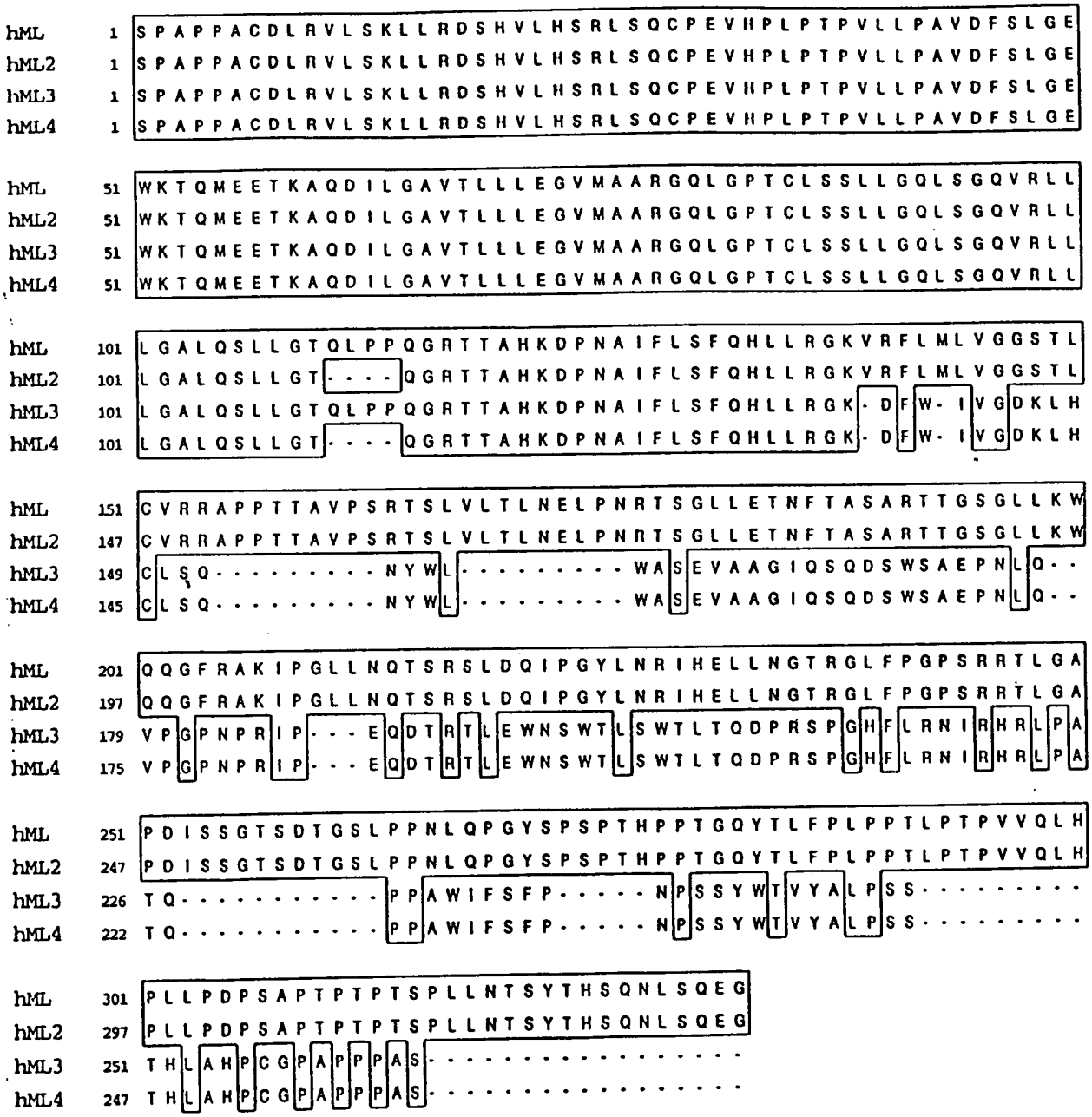

125I-HP1-1D Bound
0
10000
20000
30000
40000
No APP
APP
mpl-IgG
ANP-R-IgG
(5085,4056)
(32856,39625)
(3858,3817)
(32203,20789)

FIG. 8

```
                                                                           -10
                                                              ↓ L  L  L  V   V  M  L   L  L  T
  1 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT
    CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA

                                               10                            20
    A  R  L  T   L  S  S   P  A  P   P  A  C  D   L  R  V   L  S  K   L  L  R  D   S  H  V   L  H  S   R  L ↓
101 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA
    CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT

201 GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT
    CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACTGG GTTACTGATA

301 TCTTCCCATA TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA
    AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT
```

FIG. 9

FIG. 10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hML2 1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML3 1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML4 1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML2 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML3 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML4 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML 101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML2 101 LGALQSLLGT----QGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML3 101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGK-DFW-IVGDKLH
hML4 101 LGALQSLLGT----QGRTTAHKDPNAIFLSFQHLLRGK-DFW-IVGDKLH
hML 151 CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
hML2 147 CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
hML3 149 CLSQ---------NYWL---------WASEVAAGIQSQDSWSAEPNLQ--
hML4 145 CLSQ---------NYWL---------WASEVAAGIQSQDSWSAEPNLQ--
hML 201 QQGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML2 197 QQGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML3 179 VPGPNPRIP---EQDTRTLEWNSWTLSWTLTQDPRSPGHFLRNIRHRLPA
hML4 175 VPGPNPRIP---EQDTRTLEWNSWTLSWTLTQDPRSPGHFLRNIRHRLPA
hML 251 PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML2 247 PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML3 226 TQ----------PPAWIFSFP-----NPSSYWTVYALPSS---------
hML4 222 TQ----------PPAWIFSFP-----NPSSYWTVYALPSS---------
hML 301 PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML2 297 PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML3 251 THLAHPCGPAPPPAS----------
hML4 247 THLAHPCGPAPPPAS----------

FIG. 11

FIG. 12A

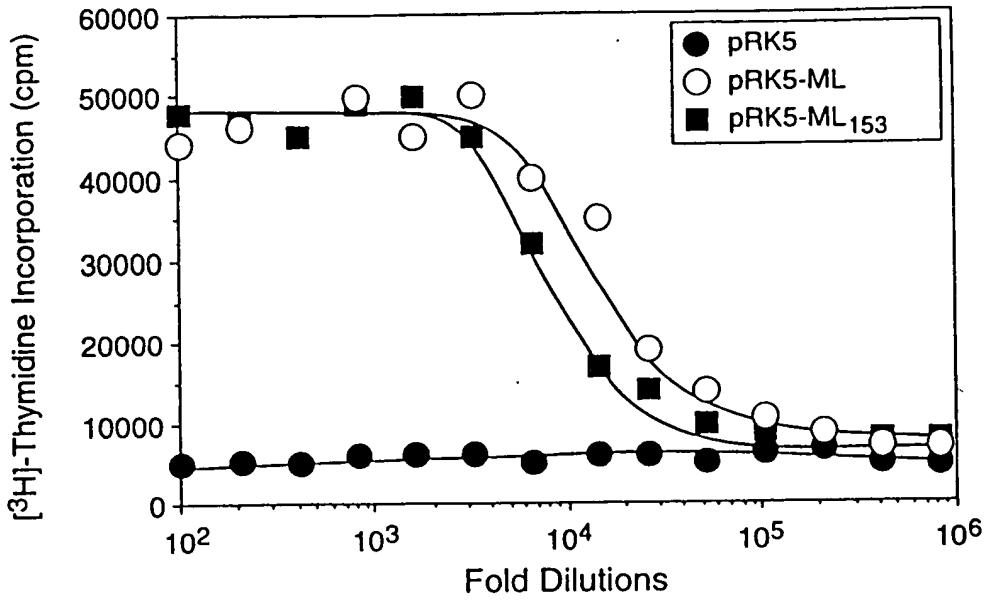


FIG. 12B

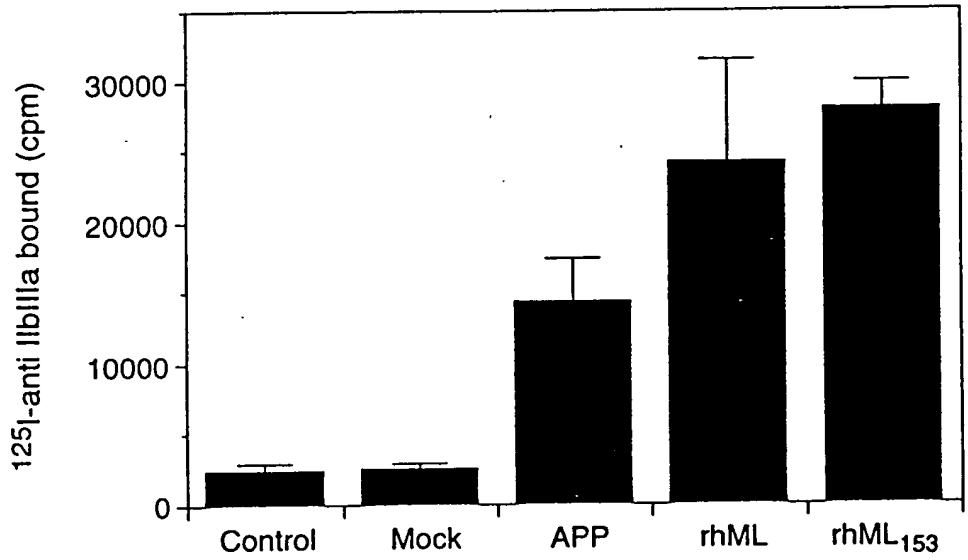
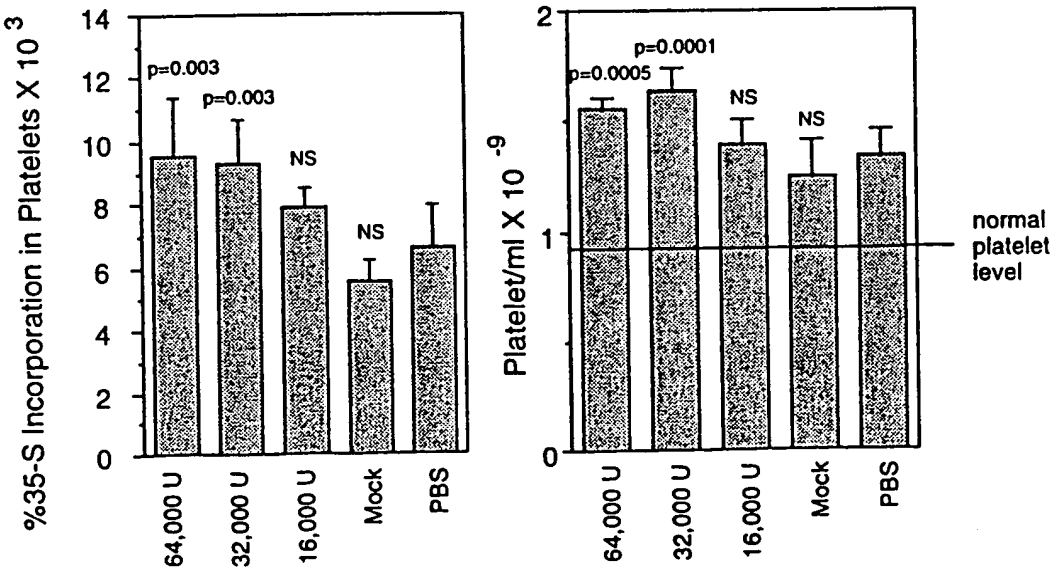


FIG. 12C



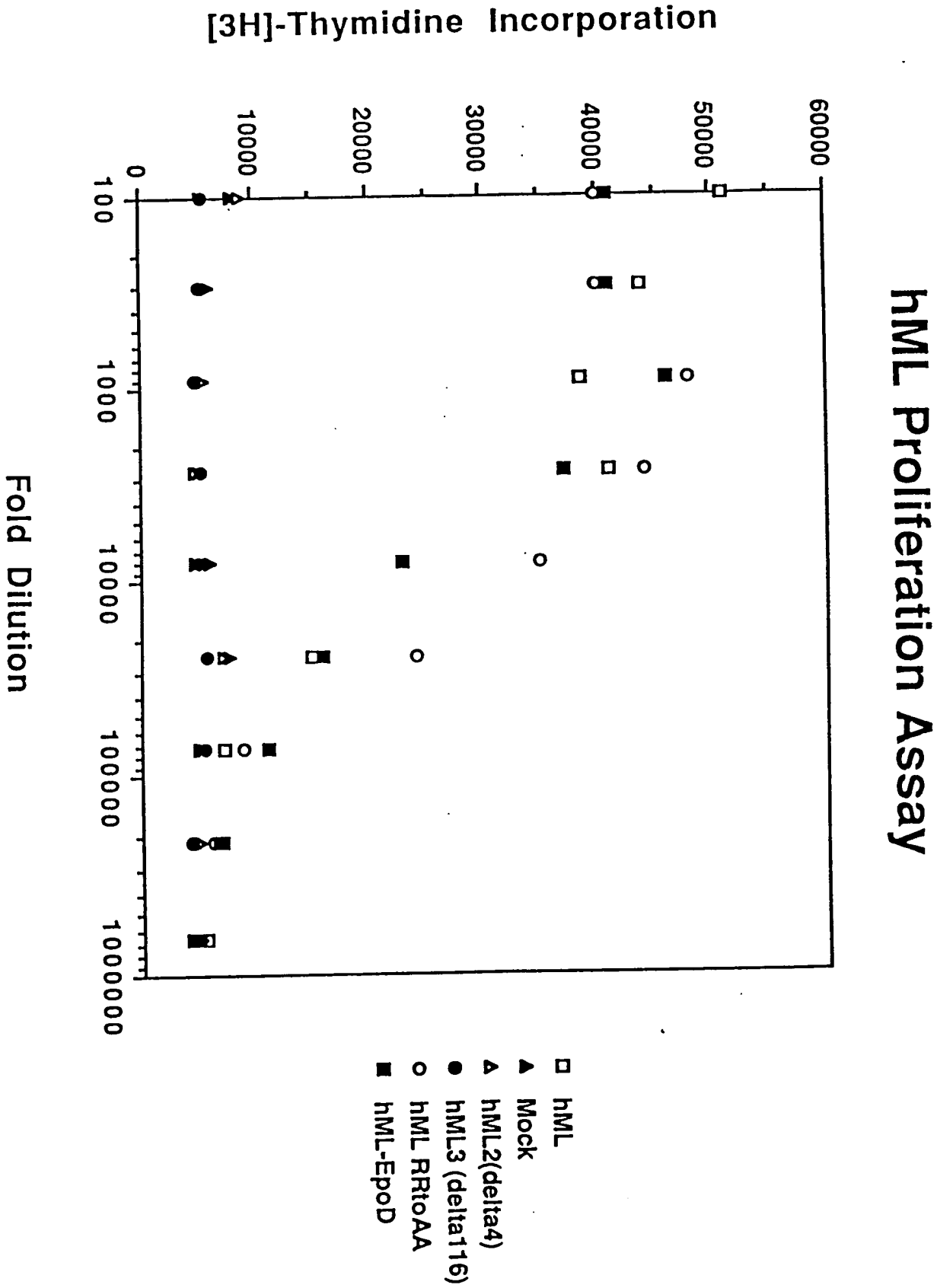

hML Proliferation Assay
[3H]-Thymidine Incorporation
0
10000
20000
30000
40000
50000
60000
Fold Dilution
100
1000
10000
100000
1000000
hML
Mock
hML2(delta4)
hML3 (delta116)
hML RRtoAA
hML-EpoD

FIG. 13

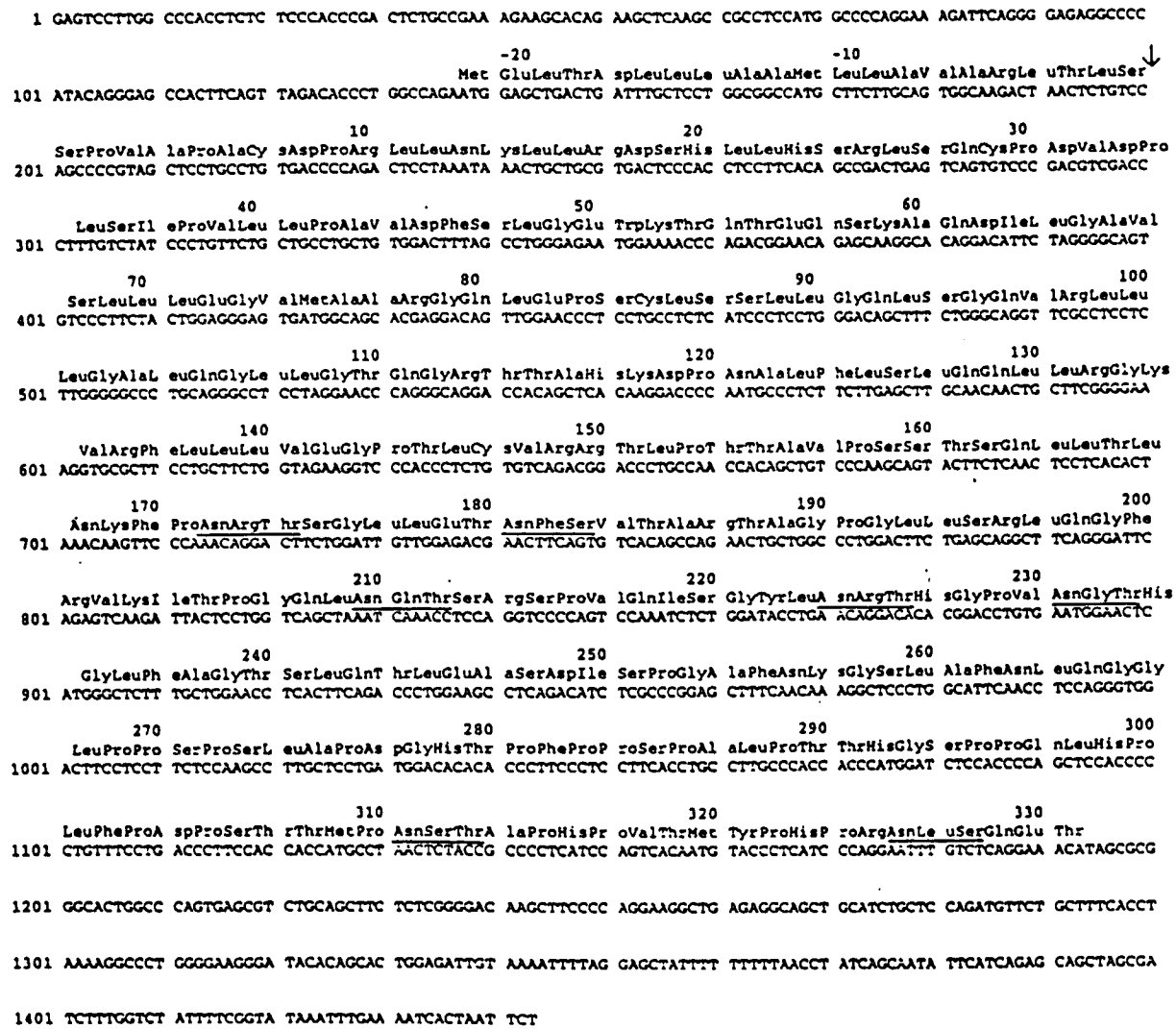


FIG. 14

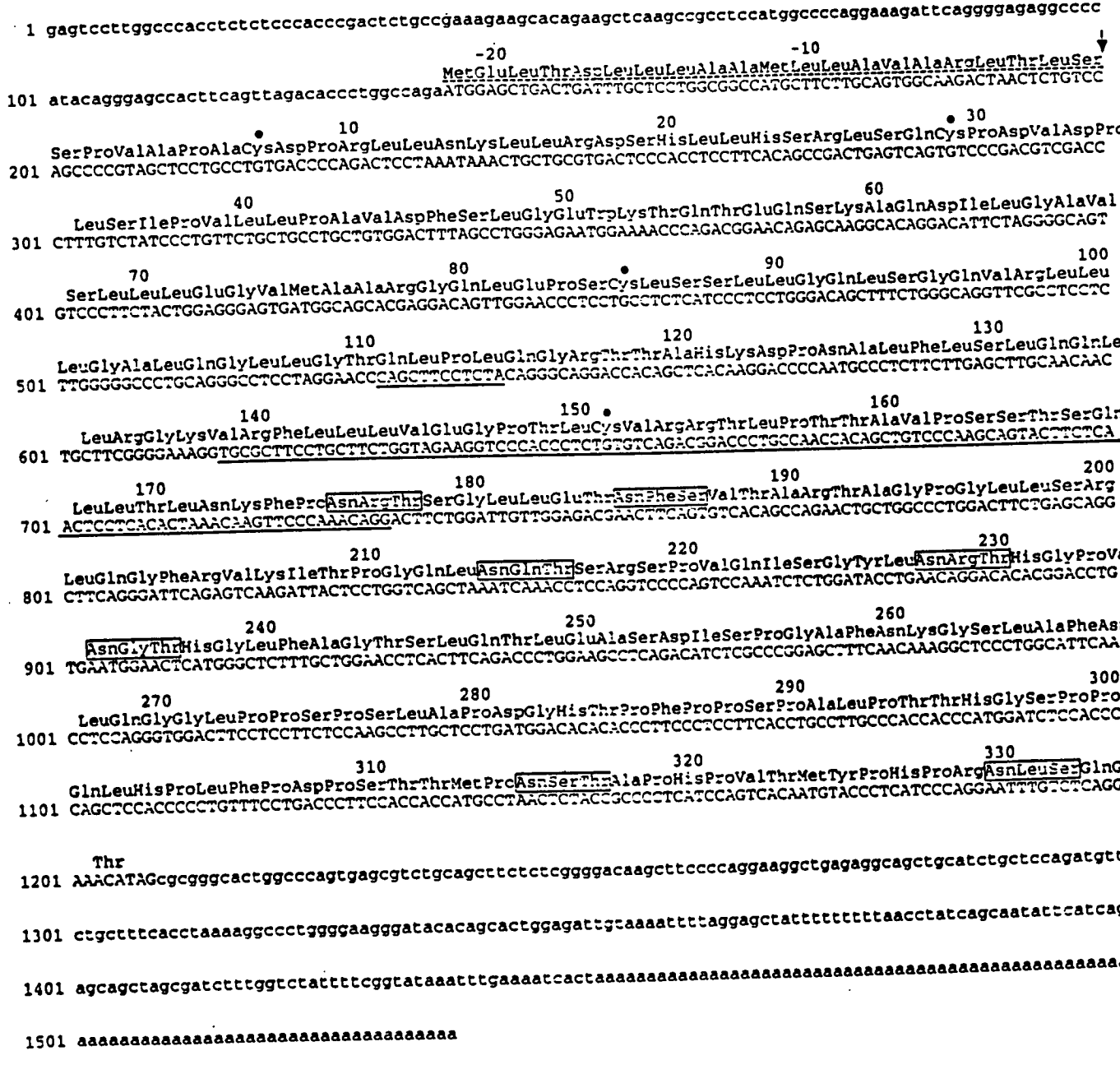
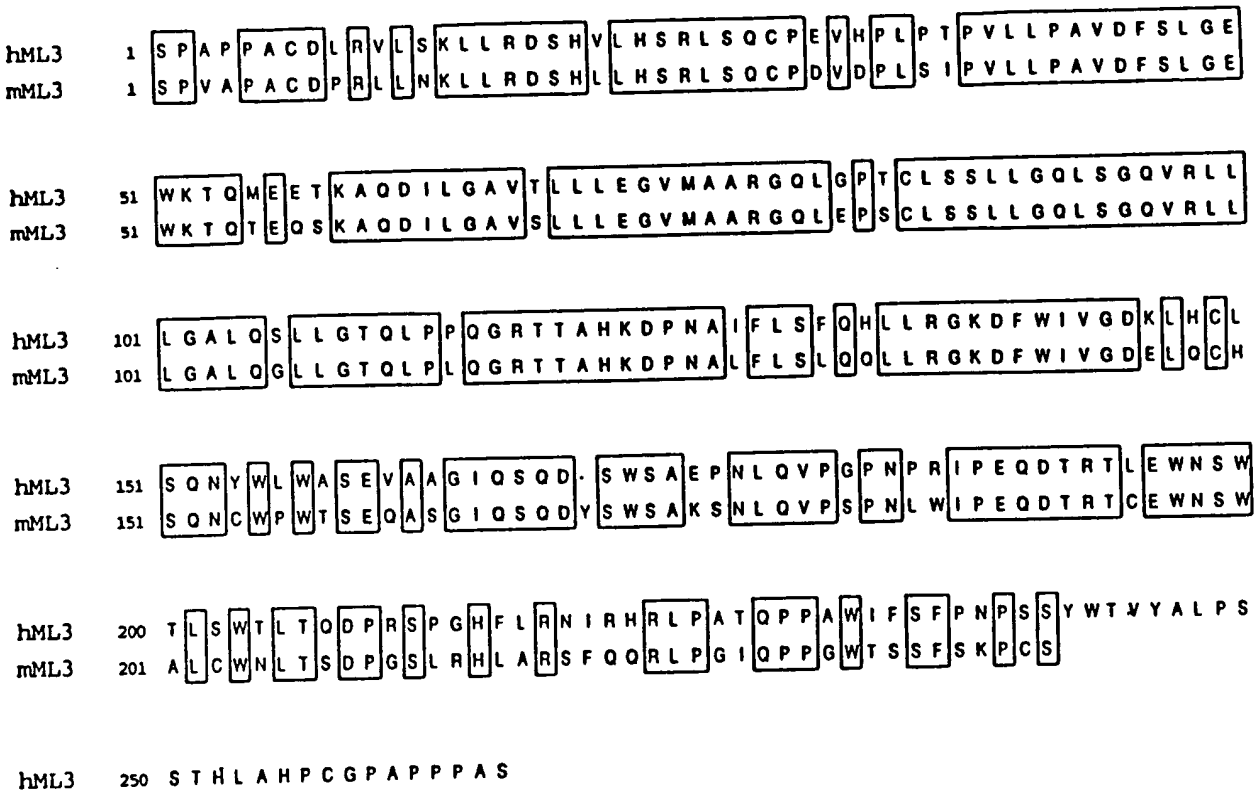


FIG. 15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mML3 1 SPVAPACDPRLLNKLLRDSHLLHSRLSQCPDVDPLSIPVLLPAVDFSLGE
hML3 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
mML3 51 WKTQTEQSKAQDILGAVSLLLEGVMAARGQLEPSCLSSLLGQLSGQVRLL
hML3 101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKDFWIVGDKLHCL
mML3 101 LGALQGLLGTQLPLQGRTTAHKDPNALFLSLQQLLRGKDFWIVGDELQCH
hML3 151 SQNYWLWASEVAAGIQSQD·SWSAEPNLQVPGPNPRIPEQDTRTLEWNSW
mML3 151 SQNCWPWTSEQASGIQSQDYSWSAKSNLQVPSPNLWIPEQDTRTCEWNSW
hML3 200 TLSWTLTQDPRSPGHFLRNIRHRLPATQPPAWIFSFPNPSSYWTWYALPS
mML3 201 ALCWNLTSDPGSLRHLARSFQQRLPGIQPPGWTSSFSKPCS
hML3 250 STHLAHPCGPAPPPAS

FIG. 16

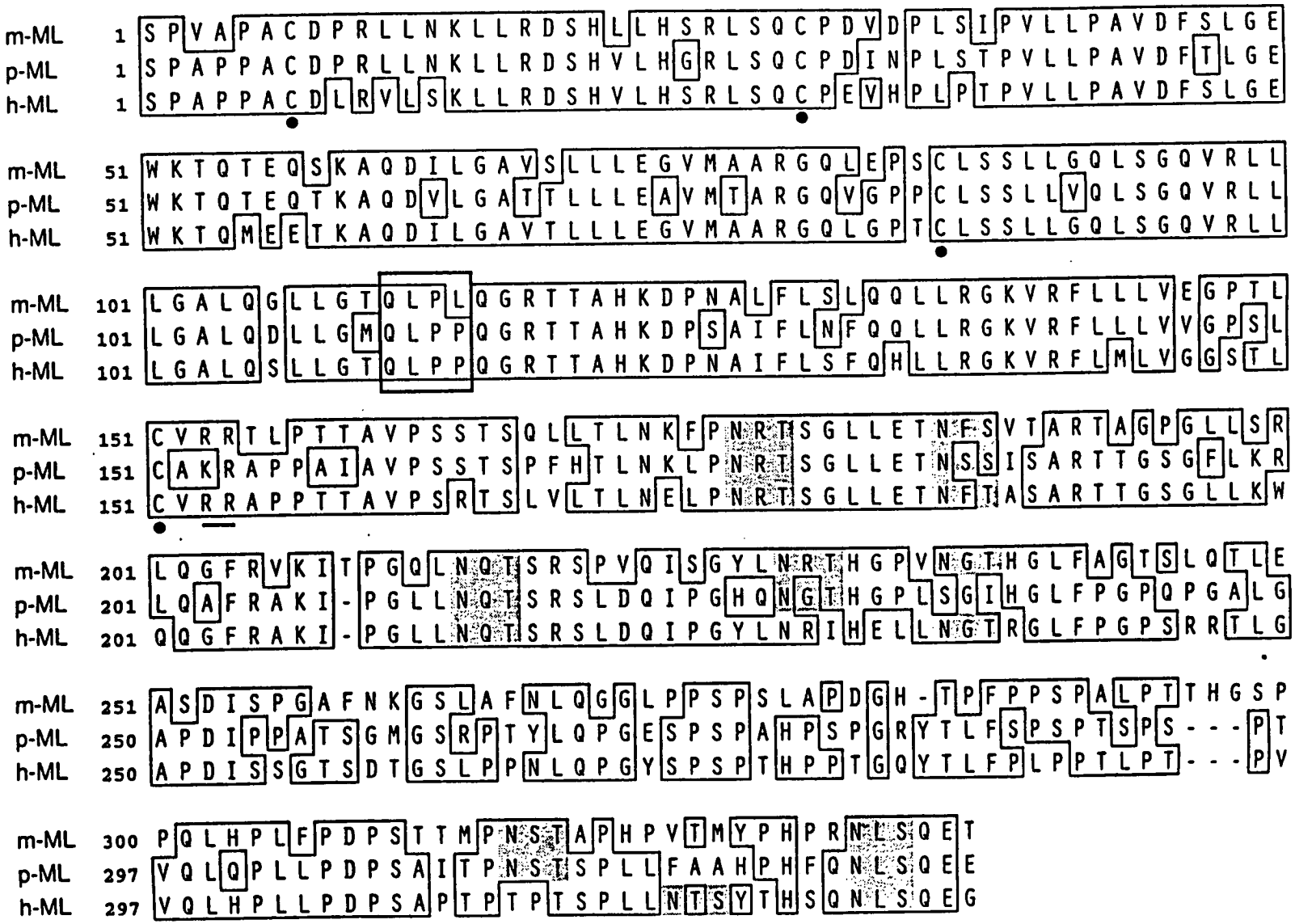

FIG. 17

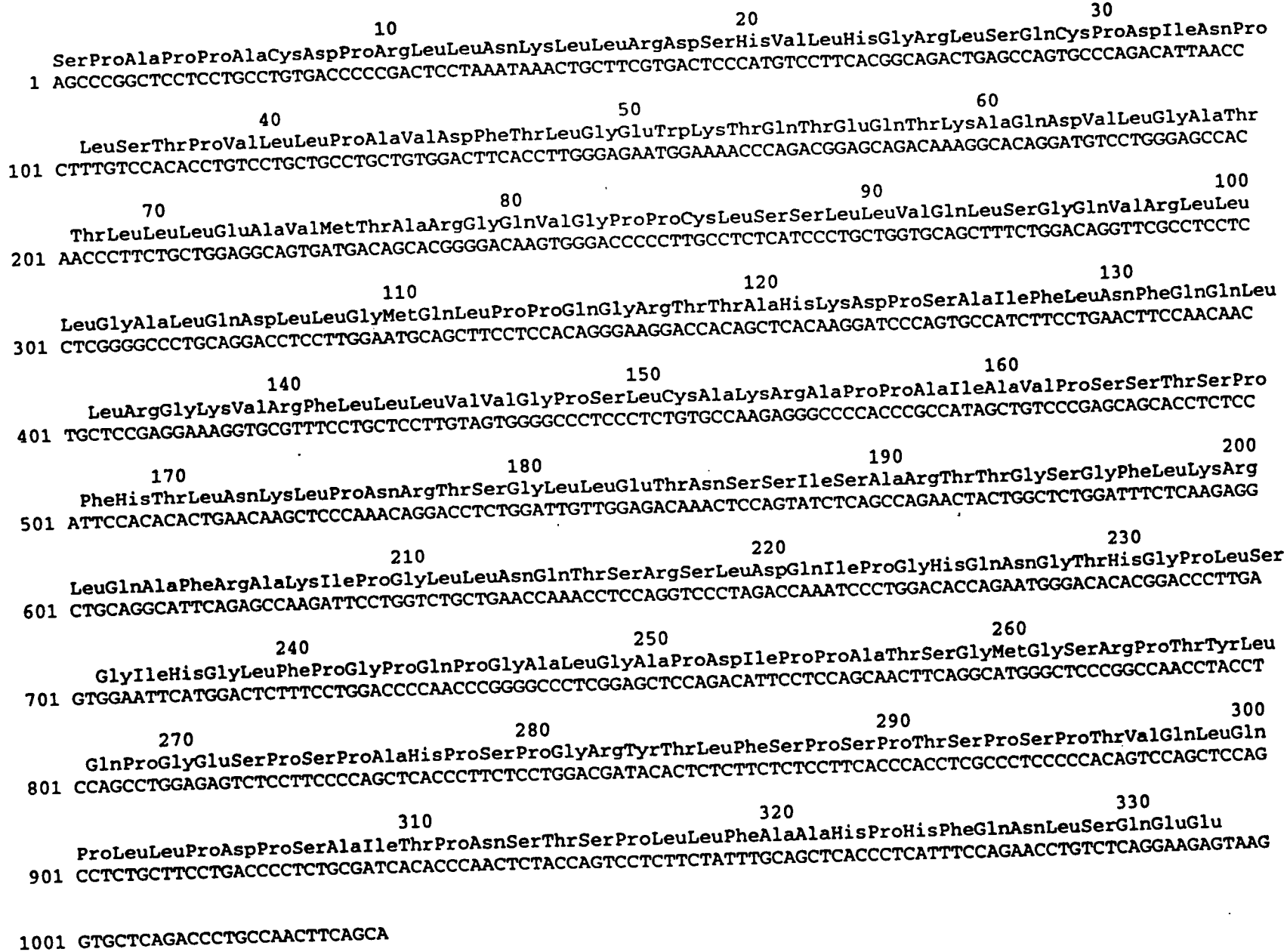

FIG. 18

```
                                10                                  20                                  30
   SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro
 1 AGCCCGGCTCCTCCTGCCTGTGACCCCCGACTCCTAAATAAACTGCTTCGTGACTCCCATGTCCTTCACGGCAGACTGAGCCAGTGCCCAGACATTAACC

                        40                                  50                                  60
     LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr
101 CTTTGTCCACACCTGTCCTGCTGCCTGCTGTGGACTTCACCTTGGGAGAATGGAAAACCCAGACGGAGCAGACAAAGGCACAGGATGTCCTGGGAGCCAC

          70                                  80                                  90                                 100
     ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu
201 AACCCTTCTGCTGGAGGCAGTGATGACAGCACGGGGACAAGTGGGACCCCCTTGCCTCTCATCCCTGCTGGTGCAGCTTTCTGGACAGGTTCGCCTCCTC

                                110                                 120                                 130
    LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeuLeuArgGlyLys
301 CTCGGGGCCCTGCAGGACCTCCTTGGAATGCAGGGAAGGACCACAGCTCACAAGGATCCCAGTGCCATCTTCCTGAACTTCCAACAACTGCTCCGAGGAA

                        140                                 150                                 160
     ValArgPheLeuLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerProPheHisThrLeu
401 AGGTGCGTTTCCTGCTCCTTGTAGTGGGGCCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCATAGCTGTCCCGAGCAGCACCTCTCCATTCCACACACT

          170                                 180                                 190                                200
     AsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArgLeuGlnAlaPhe
501 GAACAAGCTCCCAAACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTTCTCAAGAGGCTGCAGGCATTC

                                210                                 220                                 230
    ArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSerGlyIleHisGly
601 AGAGCCAAGATTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTAGACCAAATCCCTGGACACCAGAATGGGACACACGGACCCTTGAGTGGAATTCATG

                        240                                 250                                 260
     LeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeuGlnProGlyGlu
701 GACTCTTTCCTGGACCCCAACCCGGGGCCCTCGGAGCTCCAGACATTCCTCCAGCAACTTCAGGCATGGGCTCCCGGCCAACCTACCTCCAGCCTGGAGA

          270                                 280                                 290                                300
     SerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGlnProLeuLeuPro
801 GTCTCCTTCCCCAGCTCACCCTTCTCCTGGACGATACACTCTCTTCTCTCCTTCACCCACCTCGCCCTCCCCCACAGTCCAGCTCCAGCCTCTGCTTCCT

                                310                                 320
    AspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
901 GACCCCTCTGCGATCACACCCAACTCTACCAGTCCTCTTCTATTTGCAGCTCACCCTCATTTCCAGAACCTGTCTCAGGAAGAGTAAGGTGCTCAGACCC

1001 TGCCAACTTCAGCA
```

FIG. 19

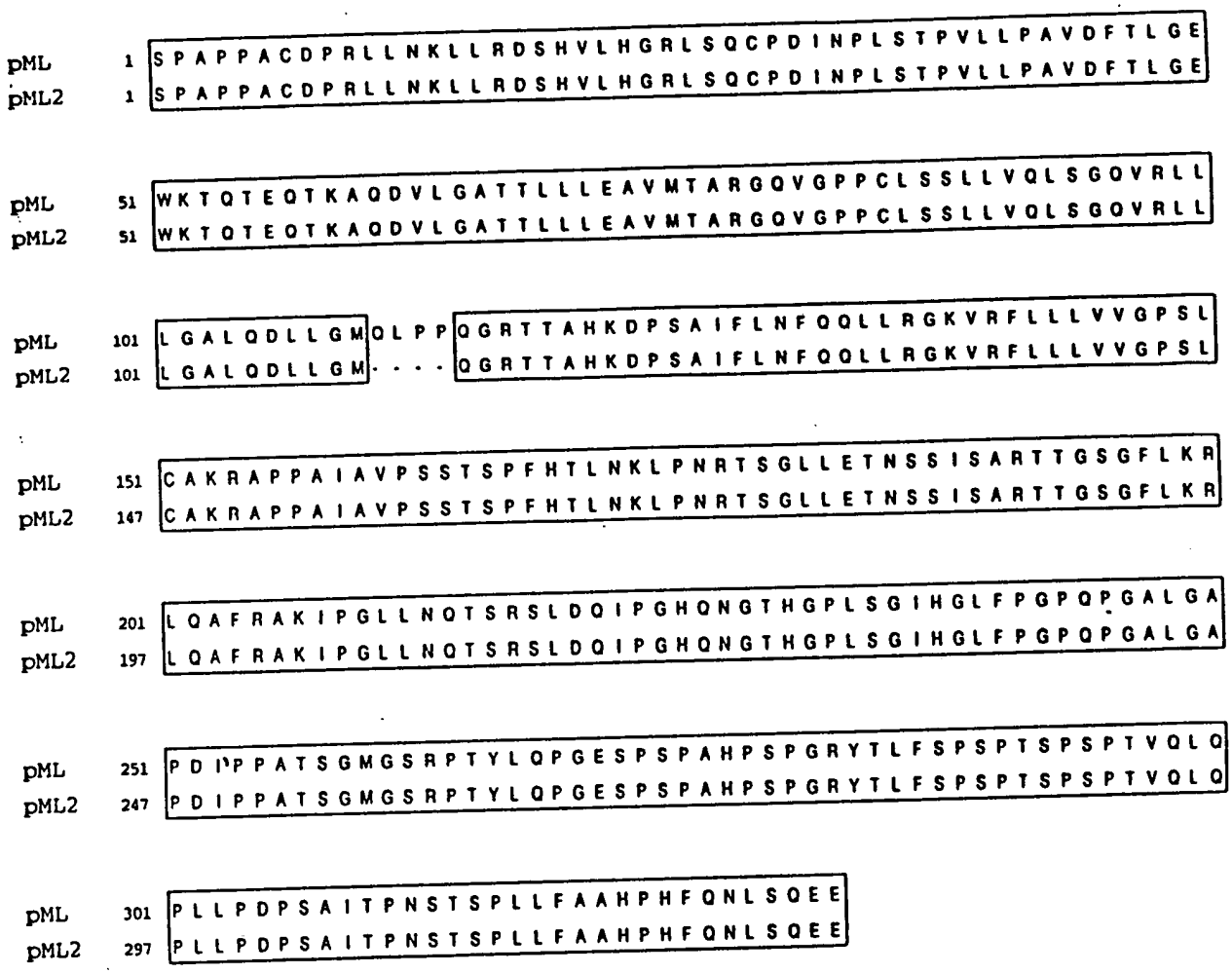
pML 1 SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE
pML2 1 SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE
pML 51 WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL
pML2 51 WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL
pML 101 LGALQDLLGMQLPPQGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL
pML2 101 LGALQDLLGM....QGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL
pML 151 CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR
pML2 147 CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR
pML 201 LQAFRAKIPGLLNQTSRSLDQIPGHQNGTHGPLSGIHGLFPGPQPGALGA
pML2 197 LQAFRAKIPGLLNQTSRSLDQIPGHQNGTHGPLSGIHGLFPGPQPGALGA
pML 251 PDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPSPTVQLQ
pML2 247 PDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPSPTVQLQ
pML 301 PLLPDPSAITPNSTSPLLFAAHPHFQNLSQEE
pML2 297 PLLPDPSAITPNSTSPLLFAAHPHFQNLSQEE

FIG. 20